

SEQUENCE LISTING

SEQ ID NO: 1

LENGTH: 524

TYPE: amino acid

TOPOLOGY: linear

KIND: peptide

SEQUENCE

Met Asn Leu His Val Val Lys Trp Lys Leu Ser Val Val Ser Val Leu
5 10 15
Ile Thr Leu Tyr Tyr Ser His Thr Val Ala Leu Ser Leu Lys Glu His
20 25 30
Leu Ala Asp Cys Leu Glu Asp Lys Asp Tyr Asp Thr Leu Leu Gln Thr
35 40 45
Leu Asp Asn Gly Leu Pro His Ile Asn Thr Ser His His Val Val Ile
50 55 60
Val Gly Ala Gly Met Ala Gly Leu Thr Ala Ala Lys Leu Leu Gln Asp
65 70 75 80
Ala Gly His Thr Val Thr Ile Leu Glu Ala Asn Asp Arg Val Gly Gly
81 85 90 95
Arg Val Glu Thr Tyr Arg Asn Glu Lys Glu Gly Trp Tyr Ala Glu Met
100 105 110
Gly Ala Met Arg Ile Pro Ser Ser His Arg Ile Val Gln Trp Phe Val
115 120 125
Lys Lys Leu Gly Val Glu Met Asn Glu Phe Val Met Thr Asp Asp Asn
130 135 140
Thr Phe Tyr Leu Val Asn Gly Val Arg Glu Arg Thr Tyr Val Val Gln
145 150 155 160
Glu Asn Pro Asp Val Leu Lys Tyr Asn Val Ser Glu Ser Glu Lys Gly
165 170 175
Ile Ser Ala Asp Asp Leu Leu Asp Arg Ala Leu Gln Lys Val Lys Glu
180 185 190
Glu Val Glu Ala Asn Gly Cys Lys Ala Ala Leu Glu Lys Tyr Asp Arg
195 200 205
Tyr Ser Val Lys Glu Tyr Leu Lys Glu Glu Gly Gly Leu Ser Pro Gly
210 215 220
Ala Val Arg Met Ile Gly Asp Leu Leu Asn Glu Gln Ser Leu Met Tyr
225 230 235 240
Thr Ala Leu Ser Glu Met Ile Tyr Asp Gln Ala Asp Val Asn Asp Ser
245 250 255
Val Thr Tyr His Glu Val Thr Gly Gly Ser Asp Leu Leu Pro Glu Ala
260 265 270
Phe Leu Ser Val Leu Asp Val Pro Ile Leu Leu Asn Ser Lys Val Lys
275 280 285

His Ile Arg Gln Ser Asp Lys Gly Val Ile Val Ser Tyr Gln Thr Gly
290 295 300
Asn Glu Ser Ser Leu Met Asp Leu Ser Ala Asp Ile Val Leu Val Thr
305 310 315 320
Thr Thr Ala Lys Ala Ala Leu Phe Ile Asp Phe Asp Pro Pro Leu Ser
325 330 335
Ile Ser Lys Met Glu Ala Leu Arg Ser Val His Tyr Asp Ser Ser Thr
340 345 350
Lys Ile Leu Leu Thr Phe Arg Asp Lys Phe Trp Glu Asp Asp Gly Ile
355 360 365
Arg Gly Gly Lys Ser Ile Thr Asp Gly Pro Ser Arg Tyr Ile Tyr Tyr
370 375 380
Pro Ser His Ser Phe His Thr Asn Glu Thr Ile Gly Val Leu Leu Ala
385 390 395 400
Ser Tyr Thr Trp Ser Asp Glu Ser Leu Leu Phe Leu Gly Ala Ser Asp
405 410 415
Glu Glu Leu Lys Glu Leu Ala Leu Arg Asp Leu Ala Lys Ile His Gly
420 425 430
Glu Gln Val Trp Asp Lys Cys Thr Gly Val Ile Val Lys Lys Trp Ser
435 440 445
Ala Asp Pro Tyr Ser Leu Gly Ala Phe Ala Leu Phe Thr Pro Tyr Gln
450 455 460
His Leu Glu Tyr Ala Gln Glu Leu Phe Ser Ser Glu Gly Arg Val His
465 470 475 480
Phe Ala Gly Glu His Thr Ala Phe Pro His Ala Trp Ile Glu Thr Ser
485 490 495
Met Lys Ser Ala Ile Arg Ala Ala Thr Asn Ile Asn Lys Val Ala Asn
500 505 510
Glu Glu Ser Thr Ile Glu His Thr Lys Asp Glu Leu
515 520

SEQ ID NO: 2
 LENGTH: 1575
 TYPE: nucleic acid
 NUMBER OF CHAIN: single strand
 TOPOLOGY: linear
 KIND: cDNA to mRNA
 SEQUENCE

ATG AAT CTG CAT GTG GTG AAA TGG AAA TTA TCT GTT GTC AGT GTG CTG	48
Met Asn Leu His Val Val Lys Trp Lys Leu Ser Val Val Ser Val Leu	
5 10 15	
ATC ACA TTG TAC TAC AGT CAC ACT GTT GCT CTC AGC CTG AAG GAA CAT	96
Ile Thr Leu Tyr Tyr Ser His Thr Val Ala Leu Ser Leu Lys Glu His	
20 25 30	
CTG GCT GAT TGT CTT GAA GAC AAA GAC TAT GAC ACG CTG CTG CAG ACT	144
Leu Ala Asp Cys Leu Glu Asp Lys Asp Tyr Asp Thr Leu Leu Gln Thr	
35 40 45	
CTG GAT AAC GGT CTT CCA CAC ATT AAC ACG TCT CAT CAT GTG GTT ATA	192
Leu Asp Asn Gly Leu Pro His Ile Asn Thr Ser His His Val Val Ile	
50 55 60	
GTC GGA GCT GCC ATG GCC GGA CTG ACG GCG GGC AAG TTA CTG CAA GAC	240
Val Gly Ala Gly Met Ala Gly Leu Thr Ala Ala Lys Leu Leu Gln Asp	
65 70 75 80	
GCA GGA CAC ACG GTA ACC ATA TTG GAG GCT AAT GAT CGT GTT GGA GGA	288
Ala Gly His Thr Val Thr Ile Leu Glu Ala Asn Asp Arg Val Gly Gly	
81 85 90 95	
CGT GTG GAG ACC TAC AGG AAT GAA AAA GAA GGC TGG TAT GCT GAA ATG	336
Arg Val Glu Thr Tyr Arg Asn Glu Lys Glu Gly Trp Tyr Ala Glu Met	
100 105 110	
GGA GCT ATG AGG ATC CCA AGC TCT CAC CGC ATC GTC CAG TGG TTT GTC	384
Gly Ala Met Arg Ile Pro Ser Ser His Arg Ile Val Gln Trp Phe Val	
115 120 125	
AAA AAG CTT GGG GTC GAG ATG AAT GAG TTC GTC ATG ACT GAT GAC AAC	432
Lys Lys Leu Gly Val Glu Met Asn Glu Phe Val Met Thr Asp Asp Asn	
130 135 140	
ACC TTT TAC CTG GTT AAT GGG GTG CGG GAG AGG ACA TAT GTT GTC CAA	480
Thr Phe Tyr Leu Val Asn Gly Val Arg Glu Arg Thr Tyr Val Val Gln	
145 150 155 160	
GAA AAC CCT GAT GTC CTG AAG TAC AAC GTG TCA GAA AGC GAG AAG GGA	528
Glu Asn Pro Asp Val Leu Lys Tyr Asn Val Ser Glu Ser Glu Lys Gly	
165 170 175	

ATT TCA GGC GAT GAT CTG CTA GAT CGA GCT TTG CAG AAG GTG AAA GAG			576
Ile Ser Ala Asp Asp Leu Leu Asp Arg Ala Leu Gln Lys Val Lys Glu			
180	185	190	
GAA GTG GAA GCA AAT GGT TGT AAA GCT GCA CTG GAA AAA TAC GAC CGC			624
Glu Val Glu Ala Asn Gly Cys Lys Ala Ala Leu Glu Lys Tyr Asp Arg			
195	200	205	
TAT TCT GTG AAG GAG TAT CTG AAA GAA GAA GGT TTG AGT GCA GGA			672
Tyr Ser Val Lys Glu Tyr Leu Lys Glu Glu Gly Leu Ser Pro Gly			
210	215	220	
GCA GTG AGG ATG ATT GGA GAC CTG CTG AAT GAA CAG AGC CTC ATG TAC			720
Ala Val Arg Met Ile Gly Asp Leu Leu Asn Glu Gln Ser Leu Met Tyr			
225	230	235	240
ACA GCG CTG AGT GAG ATG ATC TAC GAC CAG GCT GAC GTC AAT GAC AGT			768
Thr Ala Leu Ser Glu Met Ile Tyr Asp Gln Ala Asp Val Asn Asp Ser			
245	250	255	
GTC ACG TAT CAT GAA GTG ACG GGT GGA TCA GAT CTT CTT CCC GAA GCT			816
Val Thr Tyr His Glu Val Thr Gly Ser Asp Leu Leu Pro Glu Ala			
260	265	270	
TTC CTT TCT GTC CTG GAT GTC CCC ATC CTC TTA AAC TCC AAA GTC AAA			864
Phe Leu Ser Val Leu Asp Val Pro Ile Leu Leu Asn Ser Lys Val Lys			
275	280	285	
CAC ATC AGG CAG TCA GAT AAA GGT GTA ATC GTG TCA TAC CAG ACA GGC			912
His Ile Arg Gln Ser Asp Lys Gly Val Ile Val Ser Tyr Gln Thr Gly			
290	295	300	
AAT GAG TCC TCT TTG ATG GAC CTT TCT GCT GAC ATT GTT CTG GTA ACA			960
Asn Glu Ser Ser Leu Met Asp Leu Ser Ala Asp Ile Val Leu Val Thr			
305	310	315	320
ACC ACA GCA AAA GCA GCA CTC TTC ATA GAC TTT GAT CCA CCT CTC TCC			1008
Thr Thr Ala Lys Ala Ala Leu Phe Ile Asp Phe Asp Pro Pro Leu Ser			
325	330	335	
ATC AGT AAG ATG GAG GGC CTC CGG TCA GTC CAC TAT GAC AGC TOC ACT			1056
Ile Ser Lys Met Glu Ala Leu Arg Ser Val His Tyr Asp Ser Ser Thr			
340	345	350	
AAA ATC CTC CTC ACC TTT CGC GAT AAG TTC TGG GAG GAC GAT GGC ATC			1104
Lys Ile Leu Leu Thr Phe Arg Asp Lys Phe Trp Glu Asp Asp Gly Ile			
355	360	365	
CGA CGA GGC AAG AGC ATT AOC GAT GGA CCT TCT CGT TAC ATC TAC TAT			1152
Arg Gly Gly Lys Ser Ile Thr Asp Gly Pro Ser Arg Tyr Ile Tyr Tyr			
370	375	380	
CCC AGC CAC AGT TTC CAT ACA AAT GAG ACC ATT GGA GTC CTC CTG GCA			1200
Pro Ser His Ser Phe His Thr Asn Glu Thr Ile Gly Val Leu Leu Ala			
385	390	395	400

TOC TAC ACT TGG TCT GAC GAG TOC CTC CTC TTC CTG GGT GCA AGC GAT	1248		
Ser Tyr Thr Trp Ser Asp Glu Ser Leu Leu Phe Leu Gly Ala Ser Asp			
405	410	415	
GAA GAG CTG AAA GAG CTG GGC CTG AGA GAT CTG GCA AAA ATC CAC GGT	1296		
Glu Glu Leu Lys Glu Leu Ala Leu Arg Asp Leu Ala Lys Ile His Gly			
420	425	430	
GAG CAA GTC TGG GAT AAG TGC ACG GGA GTC ATA GTG AAG AAG TGG AGC	1344		
Glu Gln Val Trp Asp Lys Cys Thr Gly Val Ile Val Lys Lys Trp Ser			
435	440	445	
GCT GAT CCT TAC AGC TTG GGC GGC TTC GCT CTC TTC ACA CCC TAC CAA	1392		
Ala Asp Pro Tyr Ser Leu Gly Ala Phe Ala Leu Phe Thr Pro Tyr Gln			
450	455	460	
CAC TTG GAG TAC GCT CAG GAG CTC TTC AGC AGC GAG GGC AGG GTG CAC	1440		
His Leu Glu Tyr Ala Gln Glu Leu Phe Ser Ser Glu Gly Arg Val His			
465	470	475	480
TTT GCT GGT GAA CAC ACA GGC TTC CCT CAT GCT TGG ATC GAA ACG TCT	1488		
Phe Ala Gly Glu His Thr Ala Phe Pro His Ala Trp Ile Glu Thr Ser			
485	490	495	
ATG AAA TCT GCA ATC AGG GCT GCT ACA AAT ATT AAT AAA GTG GCA AAT	1536		
Met Lys Ser Ala Ile Arg Ala Ala Thr Asn Ile Asn Lys Val Ala Asn			
500	505	510	
GAA GAG TCA ACT ATA GAA CAT ACA AAA GAT GAG CTG TAG	1575		
Glu Glu Ser Thr Ile Glu His Thr Lys Asp Glu Leu			
515	520		